

RESULT 1
US-09-818-780-89
; Sequence 89, Application US/09818780
; Patent No. 6677146
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
; FILE REFERENCE: 1794.0030004
; CURRENT APPLICATION NUMBER: US/09/818,780
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,736
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-09-818-780-89

Query Match 100.0%; Score 1570; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.6e-142;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTKTAFEFAKGILCKENVPWGCSCPCKHVN 60
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Db 1 MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTKTAFEFAKGILCKENVPWGCSCPCKHVN 60

Qy 61 ELEEAFFKGEIEDFKVYKDKGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
|||||||
Db 61 ELEEAFFKGEIEDFKVYKDKGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120

Qy 121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILITNRRSAILPTILSRFQV 180
|||||||
Db 121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILITNRRSAILPTILSRFQV 180

Qy 181 EFKGFSVKEVMEIAKVDDEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPPLKVKLAS 240
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Db 181 EFKGFSVKEVMEIAKVDDEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPPLKVKLAS 240

Qy 241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLDTIRLFKDGLARGVNEPLWLFTL 300
|||||||
Db 241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLDTIRLFKDGLARGVNEPLWLFTL 300

Qy 301 AVQAD 305
|||||
Db 301 AVQAD 305

RESULT 1
D70432
conserved hypothetical protein aq_1526 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70432

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: D70432
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-305
 A;Cross-references: UNIPROT:O67486; UNIPARC:UPI000004350C; GB:AE000744; NID:g2983891; PIDN: AAC07454.1; PID:g2983903; GB:AE000657
 A;Experimental source: strain VF5
 C;Genetics:
 A;Gene: aq_1526

Query Match 100.0%; Score 1570; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.8e-92;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEKVFLEKLQKTLHIPGGLLFYKGEGSKTKTAFEFAKGILCKENVPWGCSCPCKHVN	60
Db	1 MEKVFLEKLQKTLHIPGGLLFYKGEGSKTKTAFEFAKGILCKENVPWGCSCPCKHVN	60
Qy	61 ELEEAFFKGEIEDFKVYKDKGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV	120
Db	61 ELEEAFFKGEIEDFKVYKDKGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV	120
Qy	121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRQV	180
Db	121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRQV	180
Qy	181 EFKGFSVKEVMEIAKVDDEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVKLAS	240
Db	181 EFKGFSVKEVMEIAKVDDEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVKLAS	240
Qy	241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKDNYTLLDTIRLFKDGLARGVNEPLWLFTL	300
Db	241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKDNYTLLDTIRLFKDGLARGVNEPLWLFTL	300
Qy	301 AVQAD 305	
Db	301 AVQAD 305	

RESULT 1

067486 AOUAE

ID 067486 AQUAE PRELIMINARY PRT: 305 AA-

ID 067486
AC 067486:

RT 01-AUG-1998 (TrEMBL rel 07; Created)

BT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DI 01-AUG-1998 (TrEMBL rel. 0), Last sequence update
DT 01-OCT-2003 (TrEMBL rel. 25, Last annotation update)

DE Hypothetical protein ag_1526

DE Hypothetical protein aq_15
CN OrderedList@Names=3Q_1536;

GN OrderedLocusNames
GS Aquifex aeolicus

US *Aquifex aeolicus*.
OC Bacteria; Aquificae; Aquificalos; Aquificaceae; Aquifex

OX NCBI_TaxID=63363;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 DR EMBL; AE000744; AAC07454.1; -; Genomic_DNA.
 DR PIR; D70432; D70432.
 DR HSSE; P06710; INJF.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR SMART; SM00382; AAA; 1.
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
 SQ SEQUENCE 305 AA; 34897 MW; 2B207935455B7E8A CRC64;

Query Match 100.0%; Score 1570; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.5e-91;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVFLELKQKTLHIPGGLLFYKGEGSGKTKTAFEFAKGILCKENPVWGGCSCPCKHVN 60
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 Db 1 MEKVFLELKQKTLHIPGGLLFYKGEGSGKTKTAFEFAKGILCKENPVWGGCSCPCKHVN 60

Qy 61 ELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
 |||||||
 Db 61 ELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120

Qy 121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFLITLTNRRSAILPTILSRIFQV 180
 |||||||
 Db 121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFLITLTNRRSAILPTILSRIFQV 180

Qy 181 EFKGFSVKEVMEIAKVDDEIAKLSGGSLKRAILLKENKDILNKVKEFLENELPKVYKLAS 240
 |||||||
 Db 181 EFKGFSVKEVMEIAKVDDEIAKLSGGSLKRAILLKENKDILNKVKEFLENELPKVYKLAS 240

Qy 241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300
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 Db 241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300

Qy 301 AVQAD 305
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 Db 301 AVQAD 305

STN SEARCH:

(FILE 'HOME' ENTERED AT 14:57:48 ON 01 DEC 2008)

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOTECHNO, EMBASE, JAPIO' ENTERED AT
15:00:53 ON 01 DEC 2008

L1 217 S AQUIFEX AND POLYMERASE

L2 110 DUP REM L1 (107 DUPLICATES REMOVED)

L3 9 S L2 AND DELTA